



27

SEQUENCE LISTING

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<110> Yamamoto, H. et al.

Sub
H1

<120> Plant Vde Genes and Methods Related Thereto

<130> 16619/03/US

<140> US 09/075,375

<141> 1998-07-05

<150> US 08/747,574

<151> 1996-11-07

<150> PCT/US96/18291

<151> 1996-11-07

<150> US 60/023,502

<151> 1996-08-06

<150> US 60/006,315

<151> 1995-11-07

<160> 9

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taagcttcaa gtactccgat cgtcaggtgg cctttggaag ccaacaaact ggct atg60
120
180
237
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5 10 15

285

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Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly Gln

333

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25

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Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe Ser	
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70 75 80	
agt ttt gag gaa ata caa aga ttt gat ctc aaa agg ggc atg act ttg	525
Ser Phe Glu Glu Ile Gln Arg Phe Asp Leu Lys Arg Gly Met Thr Leu	
85 90 95	
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Ile Leu Glu Lys Gln Trp Arg Gln Phe Ile Gln Leu Ala Ile Val Leu	
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gtt tgc aca ttt gtt atc gtt ccc aga gtt gat gcc gtt gat gct ctt	621
Val Cys Thr Phe Val Ile Val Pro Arg Val Asp Ala Val Asp Ala Leu	
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Lys Thr Cys Ala Cys Leu Leu Lys Glu Cys Arg Ile Glu Leu Ala Lys	
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230 235 240	
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Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Phe Thr Arg				
tct gct gtg caa aca ttt gtt caa gat cca gat ctt cct gga gca ctt	275	280	285	1101
Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala Leu				
tat aat cat gac aat gag ttt ctt cac tac caa gat gac tgg tac ata	290	295	300	1149
Tyr Asn His Asp Asn Glu Phe Leu His Tyr Gln Asp Asp Trp Tyr Ile				
tta tct tcc caa atc gaa aac aaa ccc gat gat tac ata ttc gta tac	310	315	320	1197
Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val Tyr				
tac cga ggt cga aac gac gca tgg gat gga tac ggt ggg tcc gtg atc	325	330	335	1245
Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Ser Val Ile				
tac acc cga agc ccg aca ctc ccc gaa tcg atc atc cca aac cta caa	340	345	350	1293
Tyr Thr Arg Ser Pro Thr Leu Pro Glu Ser Ile Ile Pro Asn Leu Gln				
aaa gca gcc aaa tcc gtg ggt cga gac ttt aac aat ttc ata aca acc	355	360	365	1341
Lys Ala Ala Lys Ser Val Gly Arg Asp Phe Asn Asn Phe Ile Thr Thr				
gac aat agt tgt ggg cct gag cct cca ttg gtg gaa agg ctt gag aaa	370	375	380	1389
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aca gcg gaa gag ggc gag aag ttg ttg ata aaa gaa gct gta gag ata	390	395	400	1437
Thr Ala Glu Glu Gly Glu Lys Leu Leu Ile Lys Glu Ala Val Glu Ile				
gaa gaa gag gtt gaa aaa gag gtg gag aag gtt aga gat act gag atg	405	410	415	1485
Glu Glu Val Glu Val Glu Lys Val Arg Asp Thr Glu Met				
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Thr Leu Phe Gln Arg Leu Leu Glu Gly Phe Lys Glu Leu Gln Gln Asp				
gaa gag aat ttt gtg agg gag ttg agt aaa gaa gag aag gaa att ctg	435	440	445	1581
Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Glu Lys Glu Ile Leu				
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Ala Leu Pro Ile Arg Lys Leu Arg	
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gccgggttgc gggtaggccc aaatttttg gggccggatc ggtcttgatc gggttttct	1923
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Tyr Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe	
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100 105 110	
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130 135 140	
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145 150 155 160	
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Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Gly Glu Phe Pro	
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Ser Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala	
225 230 235 240	
Phe Asp Cys Gln Leu His Glu Phe His Met Glu Asn Asp Lys Leu Val	
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Gly Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Phe Thr	
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Arg Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala	
275 280 285	
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290 295 300	
Ile Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val	

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					420				425					430	
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 His Ser Asn Phe Leu Ala Asn His Glu Thr Ile Lys Tyr Tyr Val Gly
 10 15 20

tca aag ctt ccc ggt cat aaa agg ttt agc tgg ggt tgg gaa gat tac 152
 Ser Lys Leu Pro Gly His Lys Arg Phe Ser Trp Gly Trp Glu Asp Tyr
 25 30 35

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Phe Gly Ser Ile Val Val Ala Lys Ile Cys Ser Ser Arg Arg Ile Pro
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Arg Tyr Phe Arg Lys Ser Pro Arg Ile Cys Cys Gly Leu Asp Ser Arg
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aaa gat gta gct ttg atg gtt tgg gag aaa tgg ggc caa ttt gcc aaa Lys Asp Val Ala Leu Met Val Trp Glu Lys Trp Gly Gln Phe Ala Lys 105 110 115	392
aca gca att gta gct ata ttc att ttg tca gtt gct tca aaa gct gat Thr Ala Ile Val Ala Ile Phe Ile Leu Ser Val Ala Ser Lys Ala Asp 120 125 130	440
gcg gtt gat gct ctc aag act tgt act tgc tta ctg aaa gag tgc agg Ala Val Asp Ala Leu Lys Thr Cys Thr Cys Leu Leu Lys Glu Cys Arg 135 140 145	488
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65 70 75 80
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Gly Cys Lys Phe Pro Lys Asp Val Ala Leu Met Val Trp Glu Lys Trp
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Gly Gln Phe Ala Lys Thr Ala Ile Val Ala Ile Phe Ile Leu Ser Val
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Leu Lys Glu Cys Arg Leu Glu Leu Ala Lys Cys Ile Ser Asn Pro Ala
145 150 155 160
Cys Ala Ala Asn Val Ala Cys Leu Gln Thr Cys Asn Asn Arg Pro Asp
165 170 175
Glu Thr Glu Cys Gln Ile Lys Cys Gly Asp Leu Phe Glu Asn Ser Val
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Val Asp Glu Phe Asn Glu Cys Ala Val Ser Arg Lys Lys Cys Val Pro
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Arg Lys Ser Asp Val Gly Asp Phe Pro Val Pro Asp Pro Ser Val Leu
210 215 220
Val Gln Lys Phe Asp Met Lys Asp Phe Ser Gly Lys Trp Phe Ile Thr
225 230 235 240
Arg Gly Leu Asn Pro Thr Phe Asp Ala Phe Asp Cys Gln Leu His Glu
245 250 255
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260 265 270
Arg Thr Pro Asp Gly Gly Phe Phe Thr Arg Ser Ala Val Gln Lys Phe
275 280 285
Val Gln Asp Pro Lys Tyr Pro Gly Ile Leu Tyr Asn His Asp Asn Glu
290 295 300
Tyr Leu Leu Tyr Gln Asp Asp Trp Tyr Ile Leu Ser Ser Lys Val Glu
305 310 315 320
Asn Ser Pro Glu Asp Tyr Ile Phe Val Tyr Tyr Lys Gly Arg Asn Asp
325 330 335
Ala Trp Asp Gly Tyr Gly Ser Val Leu Tyr Thr Arg Ser Ala Val
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Leu Pro Glu Ser Ile Ile Pro Glu Leu Gln Thr Ala Ala Gln Lys Val
355 360 365
Gly Arg Asp Phe Asn Thr Phe Ile Lys Thr Asp Asn Thr Cys Gly Pro
370 375 380
Glu Pro Pro Leu Val Glu Arg Leu Glu Lys Lys Val Glu Glu Gly Glu
385 390 395 400
Arg Thr Ile Ile Lys Glu Val Glu Glu Ile Glu Glu Glu Val Glu Lys
405 410 415

Val Arg Asp Lys Glu Val Thr Leu Phe Ser Lys Leu Phe Glu Gly Phe
 420 425 430
 Lys Glu Leu Gln Arg Asp Glu Glu Asn Phe Leu Arg Glu Leu Ser Lys
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 25 30 35

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 Gly Phe Ser Lys Gly Ile Phe Asp Ile Val Pro Leu Pro Ser Lys Asn
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 85 90 95 100

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 105 110 115

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Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Leu Gly Glu Phe Pro	185	190	195	
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Val Gly Asn Ile Ser Trp Arg Ile Lys Thr Leu Asp Ser Gly Phe Phe	245	250	255	260
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Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Asn Gln Pro Gly	265	270	275	
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Val Leu Tyr Asn His Asp Asn Glu Tyr Leu His Tyr Gln Asp Asp Trp	280	285	290	
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Tyr Ile Leu Ser Ser Lys Ile Glu Asn Lys Pro Glu Asp Tyr Ile Phe	295	300	305	
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Val Tyr Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Gly Ala	310	315	320	
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Val Val Tyr Thr Arg Ser Ser Val Leu Pro Asn Ser Ile Ile Pro Glu	325	330	335	340

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Pro Ser Lys Asn Glu Leu Lys Glu Leu Thr Ala Pro Leu Leu Lys 85 90 95	
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 Ile Glu Leu Ala Lys Cys Ile Ala Asn Pro Ala Cys Ala Ala Asn Val
 130 135 140
 Ala Cys Leu Gln Thr Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln
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